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OSMM&N File No. 4625-038-55X DIV

By: JPL:SEC:mms

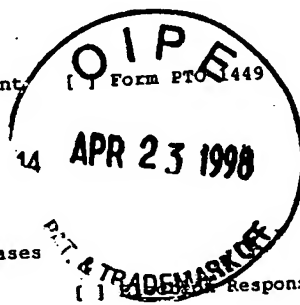
Serial No.: 08/855,531

In the Matter of the Application of: Prem S. PAUL et al.

For: VACCINES RAISING AN IMMUNOLOGICAL RESPONSE AGAINST VIRUSES CAUSING PORCINE RESPIRATORY AND REPRODUCTIVE DISEASES, METHODS OF PROTECTING A PIG AGAINST A DISEASE CAUSED BY A RESPIRATORY AND REPRODUCTIVE VIRUS, A METHOD OF PRODUCING A VACCINE WHICH RAISES AN IMMUNOLOGICAL RESPONSE AGAINST A VIRUS CAUSING A PORCINE RESPIRATORY AND REPRODUCTIVE DISEASE, AND DNA OBTAINED FROM A VIRUS CAUSING A PORCINE RESPIRATORY AND REPRODUCTIVE DISEASE

The following has been received in the U.S. Patent and Trademark Office on the date stamped hereon:

- ☐ pp. Specification & Claims/Drawings Sheets
 - ☐ Combined Declaration, Power of Attorney and Petition (pp.)
 - ☐ Utility Patent Application Transmittal
 - ☐ Fee Transmittal
 - ☐ Notice of Priority
 - ☐ Priority Doc. ()
 - ☒ Check for \$ 110.00
 - ☒ Dep. Acct. Order Form
 - ☐ Assignment Pp./Form PTO-1595
 - ☐ Letter to Official Draftsman
 - ☐ Letter Requesting Approval of Drawing Changes
 - ☐ Drawings Sheets
 - ☒ Amendment Cover Letter
 - ☒ Amendment
 - ☐ Information Disclosure Statement
 - ☒ Cited References (3)
 - ☐ Search Report
 - ☐ Statement of Relevancy
 - ☐ IDS/Related/List of Related Cases
 - ☐ Restriction Response
 - ☐ Rule 132 Declaration
 - ☒ Petition for Extension of Time (one month)
 - ☐ Notice of Appeal
 - ☒ Request for Preparation of a Computer-Readable Sequence Listing and Statement
- Due Date: April 23, 1998



BEST AVAILABLE COPY

IN RE APPLICATION OF: Prem S. PAUL et al.

SERIAL NO: 08/855,531

FILED: May 13, 1997

FOR: VACCINES RAISING AN IMMUNOLOGICAL RESPONSE AGAINST VIRUSES CAUSING PORCINE RESPIRATORY AND REPRODUCTIVE DISEASES, METHODS OF PROTECTING A PIG AGAINST A DISEASE CAUSED BY A RESPIRATORY AND REPRODUCTIVE VIRUS, A METHOD OF PRODUCING A VACCINE WHICH RAISES AN IMMUNOLOGICAL RESPONSE AGAINST A VIRUS CAUSING A PORCINE RESPIRATORY AND REPRODUCTIVE DISEASE, AND DNA OBTAINED FROM A VIRUS CAUSING A PORCINE RESPIRATORY AND REPRODUCTIVE DISEASE

ASSISTANT COMMISSIONER FOR PATENTS
WASHINGTON, D.C. 20231

Sir:

Transmitted herewith is an Amendment in the above-identified application.

- ☐ No additional fee is required.
- ☐ Small entity status of this application under 37 C.F.R. §1.9 and §1.27 has been established by a verified statement previously submitted.
- ☐ Small entity status of this application under 37 C.F.R. §1.9 and §1.27 has been established by a verified statement submitted herewith.
- ☒ Additional documents filed herewith: Petition for Extension of Time (one month); Request for Preparation of a Computer-Readable Sequence Listing and Statement; Cited References (3)

The Fee has been calculated as shown below:

	CLAIMS REMAINING AFTER		HIGHEST NUMBER PREVIOUSLY PAID FOR	NO. EXTRA CLAIMS	RATE	CALCULATIONS
TOTAL	10	MINUS	20	0	X \$ 22 =	\$0.00
INDEP	1	MINUS	3	0	X \$ 82 =	\$0.00
	MULTIPLE DEPENDENT CLAIMS				+ \$270 =	\$0.00
	TOTAL OF ABOVE CALCULATIONS =					\$0.00
	Reduction by 50% for filing by Small Entity					\$0.00
	Recordation of Assignment				+ \$ 40 =	\$0.00
	TOTAL					\$0.00

- ☒ A check in the amount of 110.00 is attached.
- ☒ Please charge any additional Fees for the papers being filed herewith and for which no check is enclosed herewith, or credit any overpayment to deposit Account No. 15-0030. A duplicate copy of this sheet is enclosed.
- ☒ If these papers are not considered timely filed by the Patent and Trademark Office, then a petition is hereby made under 37 C.F.R. §1.136, and any additional fees required under 37 C.F.R. §1.136 for any necessary extension of time may be charged to Deposit Account No. 15-0030. A duplicate copy of this sheet is enclosed.

OBLON, SPIVAK, McCLELLAND,
MAIER & NEUSTADT, P.C.

Jean-Paul Lavalleye
Attorney of Record
Registration No. 31,451

Sharon E. Crane, Ph.D.
Registration No. 36,113

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Arlington, Virginia 22202
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Facsimile (703) 413-2220
(OSMMN 1/97)

IN THE UNITED STATES PATENT & TRADEMARK OFFICE

IN RE APPLICATION OF:

Prem S. Paul et al.

: GROUP ART UNIT: 1645

SERIAL NO.: 08/855,531

: EXAMINER: CAPUTA

FILED: May 13, 1997

FOR: VACCINES RAISING AN IMMUNOLOGICAL RESPONSE AGAINST VIRUSES CAUSING PORCINE RESPIRATORY AND REPRODUCTIVE DISEASES, METHODS OF PROTECTING A PIG AGAINST A DISEASE CAUSED BY A RESPIRATORY AND REPRODUCTIVE VIRUS, A METHOD OF PRODUCING A VACCINE WHICH RAISES AN IMMUNOLOGICAL RESPONSE AGAINST A VIRUS CAUSING A PORCINE RESPIRATORY AND REPRODUCTIVE DISEASE, AND DNA OBTAINED FROM A VIRUS CAUSING A PORCINE RESPIRATORY AND REPRODUCTIVE DISEASE

PETITION FOR EXTENSION OF TIME
UNDER 37 C.F.R. §1.136

ASSISTANT COMMISSIONER FOR PATENTS
WASHINGTON, D.C. 20231

SIR:

It is hereby requested that a one month extension of time for responding to the Official Action dated December 23, 1997 be granted to April 23, 1998.

The required fee of \$ 110.00 is enclosed herewith by check and any further charges may be made against the Attorney of Record's Deposit Account No. 15-0030. A duplicate copy of this sheet is enclosed.

Respectfully submitted,

OBLON, SPIVAK, McCLELLAND,
MAIER & NEUSTADT, P.C.

Jean-Paul Lavalleye
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Registration No.: 36,113

IN THE UNITED STATES PATENT & TRADEMARK OFFICE

IN RE APPLICATION OF:

Prem S. Paul et al.

SERIAL NO.: 08/855,531

FILED: May 13, 1997

:

: GROUP ART UNIT: 1645

: EXAMINER: CAPUTA

:

FOR: VACCINES RAISING AN IMMUNOLOGICAL RESPONSE AGAINST VIRUSES CAUSING PORCINE RESPIRATORY AND REPRODUCTIVE DISEASES, METHODS OF PROTECTING A PIG AGAINST A DISEASE CAUSED BY A RESPIRATORY AND REPRODUCTIVE VIRUS, A METHOD OF PRODUCING A VACCINE WHICH RAISES AN IMMUNOLOGICAL RESPONSE AGAINST A VIRUS CAUSING A PORCINE RESPIRATORY AND REPRODUCTIVE DISEASE, AND DNA OBTAINED FROM A VIRUS CAUSING A PORCINE RESPIRATORY AND REPRODUCTIVE DISEASE

AMENDMENT

ASSISTANT COMMISSIONER FOR PATENTS
WASHINGTON, D.C. 20231

SIR:

Responsive to the Official Action dated December 23, 1998, Applicants respectfully request reconsideration in light of the following amendments and remarks.

IN THE SPECIFICATION

Page 33, lines 2 and 3, please delete "_____, _____, _____ and _____," and insert --VR 2429, VR 2428, VR 2430 and VR 2431--.

Page 94, lines 16-17, "_____, _____, _____ and _____," and insert --VR 2429, VR 2428, VR 2430 and VR 2431--.

Please replace the Sequence Listing on pages 111-130 with the following substitute Sequence Listing:

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: PAUL, PREM S.
HALBUR, PATRICK G.
MENG, XIANG-JIN
LUM, MELISSA A.
LYOO, YOUNG S.
- (ii) TITLE OF INVENTION: VACCINES RAISING AN IMMUNOLOGICAL
RESPONSE AGAINST VIRUSES CAUSING PORCINE RESPIRATORY AND
REPRODUCTIVE DISEASES, METHODS OF PROTECTING A PIG AGAINST
A DISEASE CAUSED BY A RESPIRATORY AND REPRODUCTIVE
- (iii) NUMBER OF SEQUENCES: 31
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
P.C.
 - (B) STREET: 1755 S. Jefferson Davis Highway, Suite 400
 - (C) CITY: Arlington
 - (D) STATE: Virginia
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 22202
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/131,625
 - (B) FILING DATE: 05-OCT-1993
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/969,071
 - (B) FILING DATE: 30-OCT-1992
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Lavalleye, Jean-Paul M.P.
 - (B) REGISTRATION NUMBER: 31,451
 - (C) REFERENCE/DOCKET NUMBER: 4625-016-55X CIP
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (703) 413-3000
 - (B) TELEFAX: (703) 413-2220
 - (C) TELEX: 248855 OPAT UR

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGCCGTGTG GTTCTCGCCA AT

22

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCCCATTTCC CTCTAGCGAC TG

22

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porcine reproductive and respiratory syndrome
virus

(B) STRAIN: Iowa

(C) INDIVIDUAL ISOLATE: ISU-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCGCGGAAC CATCAAGCAC

20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porcine reproductive and respiratory syndrome
virus

(B) STRAIN: Iowa

(C) INDIVIDUAL ISOLATE: ISU-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAACTTGACG CTATGTGAGC

20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porcine reproductive and respiratory syndrome
virus

(B) STRAIN: Iowa

(C) INDIVIDUAL ISOLATE: ISU-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGGTCTGGA TTGACGACAG

20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GACTGCTAGG GCTTCTGCAC

20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCCATTCAGC TCACATAGCG

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2062 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine reproductive and respiratory syndrome virus
(B) STRAIN: Iowa
(C) INDIVIDUAL ISOLATE: ISU-12

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 2..412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

G GCA GGC TTT GCT GTC CTC CAA GAC ATC AGT TGC CTT AGG CAT CGC	46
Ala Gly Phe Ala Val Leu Gln Asp Ile Ser Cys Leu Arg His Arg	
1 5 10 15	
AAC TCG GCC TCT GAG GCG ATT CGC AAA GTC CCT CAG TGC CGC ACG GCG	94
Asn Ser Ala Ser Glu Ala Ile Arg Lys Val Pro Gln Cys Arg Thr Ala	
20 25 30	
ATA GGG ACA CCC GTG TAT ATC ACT GTC ACA GCC AAT GTT ACC GAT GAG	142
Ile Gly Thr Pro Val Tyr Ile Thr Val Thr Ala Asn Val Thr Asp Glu	
35 40 45	
AAT TAT TTG CAT TCC TCT GAT CTT CTC ATG CTT TCT TCT TGC CTT TTC	190
Asn Tyr Leu His Ser Ser Asp Leu Leu Met Leu Ser Ser Cys Leu Phe	
50 55 60	
TAT GCT TCT GAG ATG AGT GAA AAG GGA TTT AAG GTG GTA TTT GGC AAT	238
Tyr Ala Ser Glu Met Ser Glu Lys Gly Phe Lys Val Val Phe Gly Asn	
65 70 75	
GTG TCA GGC ATC GTG GCA GTG TGC GTC AAC TTC ACC AGT TAC GTC CAA	286
Val Ser Gly Ile Val Ala Val Cys Val Asn Phe Thr Ser Tyr Val Gln	
80 85 90 95	
CAT GTC AAG GAA TTT ACC CAA CGT TCC TTG GTA GTT GAC CAT GTG CGG	334
His Val Lys Glu Phe Thr Gln Arg Ser Leu Val Val Asp His Val Arg	
100 105 110	
CTG CTC CAT TTC ATG ACG CCC GAG ACC ATG AGG TGG GCA ACT GTT TTA	382
Leu Leu His Phe Met Thr Pro Glu Thr Met Arg Trp Ala Thr Val Leu	
115 120 125	
GCC TGT CTT TTT GGC ATT CTG TTG GCA ATT TGAATGTTTA AGTATGTTGG	432
Ala Cys Leu Phe Gly Ile Leu Leu Ala Ile	
130 135	
GGAAATGCTT GACCGCGGGC TGTGCTCGC AATTGCTTTT TTTGTGGTGT ATCGTGCCGT	492
CTTGTTTTGT TGCCTCGTC AGCGCCAACG GGAACAGCGG CTCAAATTTA CAGCTGATTT	552

ACAACTTGAC GCTATGTGAG CTGAATGGCA CAGATTGGCT AGCTAATAAA TTTGACTGGG	612
CAGTGGAGTG TTTTGTCAATT TTTCCTGTGT TGA CTCACAT TGTCTCTTAT GGTGCCCTCA	672
CTACTAGCCA TTTCCTTGAC ACAGTCGGTC TGGTCACTGT GTCTACCGCT GGGTTTGTTC	732
ACGGGCGGTA TGTTCTGAGT AGCATGTACG CGGTCTGTGC CCTGGCTGCG TTGATTGCT	792
TCGTCATTAG GCTTGCGAAG AATTGCATGT CCTGGCGCTA CTCATGTACC AGATATACCA	852
ACTTTCTTCT GGACACTAAG GGCAGACTCT ATCGTTGGCG GTCGCCTGTC ATCATAGAGA	912
AAAGGGGCAA AGTTGAGGTC GAAGGTCACC TGATCGACCT CAAAAGAGTT GTGCTTGATG	972
GTTCCGCGGC TACCCCTGTA ACCAGAGTTT CAGCGGAACA ATGGAGTCGT CCTTAGATGA	1032
CTTCTGTCAT GATAGCACGG CTCCACAAAA GGTGCTCTTG GCGTTTTCTA TTACCTACAC	1092
GCCAGTGATG ATATATGCCC TAAAGGTGAG TCGCGGCCGA CTGCTAGGGC TTCTGCACCT	1152
TTTGGTCTTC CTGAATTGTG CTTTCACCTT CGGGTACATG ACATTCGTGC ACTTTCAGAG	1212
TACAAATAAG GTCGCGCTCA CTATGGGAGC AGTAGTTGCA CTCCTTTGGG GGGTGTACTC	1272
AGCCATAGAA ACCTGGAAAT TCATCACCTC CAGATGCCGT TTGTGCTTGC TAGGCCGCAA	1332
GTACATTCTG GCCCCTGCCC ACCACGTTGA AAGTGCCGCA GGCTTTCATC CGATTGCGGC	1392
AAATGATAAC CACGCATTTG TCGTCCGGCG TCCCGGCTCC ACTACGGTCA ACGGCACATT	1452
GGTGCCCGGG TTA AAAAGCC TCGTGTTGGG TGGCAGAAAA GCTGT TAAAC AGGGAGTGGT	1512
AAACCTTGTT AAATATGCCA AATAACACCG GCAAGCAGCA GAAGAGAAAG AAGGGGGATG	1572
GCCAGCCAGT CAATCAGCTG TGCCAGATGC TGGGTAAGAT CATCGCTCAC CAAAACCAGT	1632
CCAGAGGCAA GGGACCGGGA AAGAAAAATA AGAAGAAAAA CCCGGAGAAG CCCCATTTCC	1692
CTCTAGCGAC TGAAGATGAT GTCAGACATC ACTTTACCCC TAGTGAGCGT CAATTGTGTC	1752
TGTCGTCAAT CCAGACCGCC TTTAATCAAG GCGCTGGGAC TTGCACCCTG TCAGATTCAG	1812
GGAGGATAAG TTACTGTG GAGTTTAGTT TGCCTACGCA TCATACTGTG CGCCTGATCC	1872
GCGTCACAGC ATCACCTCA GCATGATGGG CTGGCATTCT TGAGGCATCC CAGTGT TGA	1932
ATTGGAAGAA TGCGTGGTGA ATGGCACTGA TTGACATTGT GCCTCTAAGT CACCTATTCA	1992
ATTAGGGCGA CCGTGTGGG GTAAGATTTA ATTGGCGAGA ACCACACGGC CGAAATTAAA	2052
AAAAAAAAA	2062

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Gly Phe Ala Val Leu Gln Asp Ile Ser Cys Leu Arg His Arg Asn
1 5 10 15
Ser Ala Ser Glu Ala Ile Arg Lys Val Pro Gln Cys Arg Thr Ala Ile
20 25 30
Gly Thr Pro Val Tyr Ile Thr Val Thr Ala Asn Val Thr Asp Glu Asn
35 40 45
Tyr Leu His Ser Ser Asp Leu Leu Met Leu Ser Ser Cys Leu Phe Tyr
50 55 60
Ala Ser Glu Met Ser Glu Lys Gly Phe Lys Val Val Phe Gly Asn Val
65 70 75 80
Ser Gly Ile Val Ala Val Cys Val Asn Phe Thr Ser Tyr Val Gln His
85 90 95
Val Lys Glu Phe Thr Gln Arg Ser Leu Val Val Asp His Val Arg Leu
100 105 110
Leu His Phe Met Thr Pro Glu Thr Met Arg Trp Ala Thr Val Leu Ala
115 120 125
Cys Leu Phe Gly Ile Leu Leu Ala Ile
130 135

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine reproductive and respiratory syndrome virus

(B) STRAIN: Iowa
(C) INDIVIDUAL ISOLATE: ISU-12

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG TTG GGG AAA TGC TTG ACC GCG GGC TGT TGC TCG CAA TTG CTT TTT	48
Met Leu Gly Lys Cys Leu Thr Ala Gly Cys Cys Ser Gln Leu Leu Phe	
1 5 10 15	
TTG TGG TGT ATC GTG CCG TCT TGT TTT GTT GCG CTC GTC AGC GCC AAC	96
Leu Trp Cys Ile Val Pro Ser Cys Phe Val Ala Leu Val Ser Ala Asn	
20 25 30	
GGG AAC AGC GGC TCA AAT TTA CAG CTG ATT TAC AAC TTG ACG CTA TGT	144
Gly Asn Ser Gly Ser Asn Leu Gln Leu Ile Tyr Asn Leu Thr Leu Cys	
35 40 45	
GAG CTG AAT GGC ACA GAT TGG CTA GCT AAT AAA TTT GAC TGG GCA GTG	192
Glu Leu Asn Gly Thr Asp Trp Leu Ala Asn Lys Phe Asp Trp Ala Val	
50 55 60	
GAG TGT TTT GTC ATT TTT CCT GTG TTG ACT CAC ATT GTC TCT TAT GGT	240
Glu Cys Phe Val Ile Phe Pro Val Leu Thr His Ile Val Ser Tyr Gly	
65 70 75 80	
GCC CTC ACT ACT AGC CAT TTC CTT GAC ACA GTC GGT CTG GTC ACT GTG	288
Ala Leu Thr Thr Ser His Phe Leu Asp Thr Val Gly Leu Val Thr Val	
85 90 95	
TCT ACC GCT GGG TTT GTT CAC GGG CGG TAT GTT CTG AGT AGC ATG TAC	336
Ser Thr Ala Gly Phe Val His Gly Arg Tyr Val Leu Ser Ser Met Tyr	
100 105 110	
GCG GTC TGT GCC CTG GCT GCG TTG ATT TGC TTC GTC ATT AGG CTT GCG	384
Ala Val Cys Ala Leu Ala Ala Leu Ile Cys Phe Val Ile Arg Leu Ala	
115 120 125	
AAG AAT TGC ATG TCC TGG CGC TAC TCA TGT ACC AGA TAT ACC AAC TTT	432
Lys Asn Cys Met Ser Trp Arg Tyr Ser Cys Thr Arg Tyr Thr Asn Phe	
130 135 140	
CTT CTG GAC ACT AAG GGC AGA CTC TAT CGT TGG CGG TCG CCT GTC ATC	480
Leu Leu Asp Thr Lys Gly Arg Leu Tyr Arg Trp Arg Ser Pro Val Ile	
145 150 155 160	

ATA GAG AAA AGG GGC AAA GTT GAG GTC GAA GGT CAC CTG ATC GAC CTC	528
Ile Glu Lys Arg Gly Lys Val Glu Val Glu Gly His Leu Ile Asp Leu	
165 170 175	
AAA AGA GTT GTG CTT GAT GGT TCC GCG GCT ACC CCT GTA ACC AGA GTT	576
Lys Arg Val Val Leu Asp Gly Ser Ala Ala Thr Pro Val Thr Arg Val	
180 185 190	
TCA GCG GAA CAA TGG AGT CGT CCT TAG	603
Ser Ala Glu Gln Trp Ser Arg Pro	
195 200	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Leu	Gly	Lys	Cys	Leu	Thr	Ala	Gly	Cys	Cys	Ser	Gln	Leu	Leu	Phe
1				5					10					15	
Leu	Trp	Cys	Ile	Val	Pro	Ser	Cys	Phe	Val	Ala	Leu	Val	Ser	Ala	Asn
			20					25					30		
Gly	Asn	Ser	Gly	Ser	Asn	Leu	Gln	Leu	Ile	Tyr	Asn	Leu	Thr	Leu	Cys
		35					40					45			
Glu	Leu	Asn	Gly	Thr	Asp	Trp	Leu	Ala	Asn	Lys	Phe	Asp	Trp	Ala	Val
	50					55					60				
Glu	Cys	Phe	Val	Ile	Phe	Pro	Val	Leu	Thr	His	Ile	Val	Ser	Tyr	Gly
65					70					75					80
Ala	Leu	Thr	Thr	Ser	His	Phe	Leu	Asp	Thr	Val	Gly	Leu	Val	Thr	Val
				85					90					95	
Ser	Thr	Ala	Gly	Phe	Val	His	Gly	Arg	Tyr	Val	Leu	Ser	Ser	Met	Tyr
			100					105					110		
Ala	Val	Cys	Ala	Leu	Ala	Ala	Leu	Ile	Cys	Phe	Val	Ile	Arg	Leu	Ala
		115					120					125			
Lys	Asn	Cys	Met	Ser	Trp	Arg	Tyr	Ser	Cys	Thr	Arg	Tyr	Thr	Asn	Phe
	130					135					140				

Leu Leu Asp Thr Lys Gly Arg Leu Tyr Arg Trp Arg Ser Pro Val Ile
 145 150 155 160
 Ile Glu Lys Arg Gly Lys Val Glu Val Glu Gly His Leu Ile Asp Leu
 165 170 175
 Lys Arg Val Val Leu Asp Gly Ser Ala Ala Thr Pro Val Thr Arg Val
 180 185 190
 Ser Ala Glu Gln Trp Ser Arg Pro
 195 200

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Lelystad

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGAGATGTT CTCACAAATT GGGGCGTTTC TTGACTCCGC ACTCTTGCTT CTGGTGGCTT	60
TTTTTGCTGT GTACCGGCTT GTCCTGGTCC TTTGCCGATG GCAACGGCGA CAGCTCGACA	120
TACCAATACA TATATAACTT GACGATATGC GAGCTGAATG GGACCGACTG GTTGTCCAGC	180
CATTTTGGTT GGGCAGTCGA GACCTTTGTG CTTTACCCGG TTGCCACTCA TATCCTCTCA	240
CTGGGTTTTT TCACAACAAG CCATTTTTTT GACGCGCTCG GTCTCGGCGC TGTATCCACT	300
GCAGGATTTG TTGGCGGGCG GTACGTAATC TGCAGCGTCT ACGGCGCTTG TGCTTTCGCA	360
CGGTCGTAT GTTTTGTCAT CCGTGCTGCT AAAAATTGCA TGGCCTGCCG CTATGCCCCG	420
ACCCGGTTTA CCAACTTCAT TGTGGACGAC CGGGGGAGAG TTCATCGATG GAAGTCTCCA	480
ATAGTGGTAG AAAAATTGGG CAAAGCCGAA GTCGATGGCA ACCTCGTCAC CATCAAACAT	540
GTCGTCCTCG AAGGGGTAA AGCTCAACCC TTGACGAGGA CTTCGGCTGA GCAATGGGAG	600
GCCTAG	606

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

A ATG GAG TCG TCC TTA GAT GAC TTC TGT CAT GAT AGC ACG GCT CCA	46
Met Glu Ser Ser Leu Asp Asp Phe Cys His Asp Ser Thr Ala Pro	
1 5 10 15	
CAA AAG GTG CTC TTG GCG TTT TCT ATT ACC TAC ACG CCA GTG ATG ATA	94
Gln Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile	
20 25 30	
TAT GCC CTA AAG GTG AGT CGC GGC CGA CTG CTA GGG CTT CTG CAC CTT	142
Tyr Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu His Leu	
35 40 45	
TTG GTC TTC CTG AAT TGT GCT TTC ACC TTC GGG TAC ATG ACA TTC GTG	190
Leu Val Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Val	
50 55 60	
CAC TTT CAG AGT ACA AAT AAG GTC GCG CTC ACT ATG GGA GCA GTA GTT	238
His Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val	
65 70 75	
GCA CTC CTT TGG GGG GTG TAC TCA GCC ATA GAA ACC TGG AAA TTC ATC	286
Ala Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile	
80 85 90 95	
ACC TCC AGA TGC CGT TTG TGC TTG CTA GGC CGC AAG TAC ATT CTG GCC	334
Thr Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala	
100 105 110	

CCT GCC CAC CAC GTT GAA AGT GCC GCA GGC TTT CAT CCG ATT GCG GCA	382
Pro Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala	
115 120 125	
AAT GAT AAC CAC GCA TTT GTC GTC CGG CGT CCC GGC TCC ACT ACG GTC	430
Asn Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val	
130 135 140	
AAC GGC ACA TTG GTG CCC GGG TTA AAA AGC CTC GTG TTG GGT GGC AGA	478
Asn Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg	
145 150 155	
AAA GCT GTT AAA CAG GGA GTG GTA AAC CTT GTT AAA TAT GCC AAA TAA	526
Lys Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys	
160 165 170	

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Glu	Ser	Ser	Leu	Asp	Asp	Phe	Cys	His	Asp	Ser	Thr	Ala	Pro	Gln
1				5					10					15	
Lys	Val	Leu	Leu	Ala	Phe	Ser	Ile	Thr	Tyr	Thr	Pro	Val	Met	Ile	Tyr
		20						25					30		
Ala	Leu	Lys	Val	Ser	Arg	Gly	Arg	Leu	Leu	Gly	Leu	Leu	His	Leu	Leu
		35					40					45			
Val	Phe	Leu	Asn	Cys	Ala	Phe	Thr	Phe	Gly	Tyr	Met	Thr	Phe	Val	His
	50					55					60				
Phe	Gln	Ser	Thr	Asn	Lys	Val	Ala	Leu	Thr	Met	Gly	Ala	Val	Val	Ala
	65				70					75					80
Leu	Leu	Trp	Gly	Val	Tyr	Ser	Ala	Ile	Glu	Thr	Trp	Lys	Phe	Ile	Thr
			85						90					95	
Ser	Arg	Cys	Arg	Leu	Cys	Leu	Leu	Gly	Arg	Lys	Tyr	Ile	Leu	Ala	Pro
			100					105					110		
Ala	His	His	Val	Glu	Ser	Ala	Ala	Gly	Phe	His	Pro	Ile	Ala	Ala	Asn
			115				120						125		

Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn
 130 135 140
 Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys
 145 150 155 160
 Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys
 165 170

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Lelystad

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGGGAGGCC TAGACGATTT TTGCAACGAT CCTATCGCCG CACAAAAGCT CGTGCTAGCC	60
TTTAGCATCA CATAACACC TATAATGATA TACGCCCTTA AGGTGTCACG CGGCCGACTC	120
CTGGGGCTGT TGCACATCCT AATATTTCTG AACTGTTCTT TTACATTCGG ATACATGACA	180
TATGTGCATT TTCAATCCAC CAACCGTGTC GCACTTACCC TGGGGGCTGT TGTCGCCCTT	240
CTGTGGGGTG TTTACAGCTT CACAGAGTCA TGGAAGTTTA TCACTTCCAG ATGCAGATTG	300
TGTTGCCTTG GCCGGCGATA CATTCTGGCC CCTGCCCATC ACGTAGAAAG TGCTGCAGGT	360
CTCCATTCAA TCTCAGCGTC TGGTAACCGA GCATACGCTG TGAGAAAGCC CGGACTAACA	420
TCAGTGAACG GCACTCTAGT ACCAGGACTT CGGAGCCTCG TGCTGGGCGG CAAACGAGCT	480
GTAAACGAG GAGTGGTTAA CCTCGTCAAG TATGGCCGGT AA	522

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porcine reproductive and respiratory syndrome virus

(B) STRAIN: Iowa

(C) INDIVIDUAL ISOLATE: ISU-12

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATG CCA AAT AAC ACC GGC AAG CAG CAG AAG AGA AAG AAG GGG GAT GGC	48
Met Pro Asn Asn Thr Gly Lys Gln Gln Lys Arg Lys Lys Gly Asp Gly	
1 5 10 15	
CAG CCA GTC AAT CAG CTG TGC CAG ATG CTG GGT AAG ATC ATC GCT CAC	96
Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala His	
20 25 30	
CAA AAC CAG TCC AGA GGC AAG GGA CCG GGA AAG AAA AAT AAG AAG AAA	144
Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys	
35 40 45	
AAC CCG GAG AAG CCC CAT TTC CCT CTA GCG ACT GAA GAT GAT GTC AGA	192
Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg	
50 55 60	
CAT CAC TTT ACC CCT AGT GAG CGT CAA TTG TGT CTG TCG TCA ATC CAG	240
His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln	
65 70 75 80	
ACC GCC TTT AAT CAA GGC GCT GGG ACT TGC ACC CTG TCA GAT TCA GGG	288
Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly	
85 90 95	
AGG ATA AGT TAC ACT GTG GAG TTT AGT TTG CCT ACG CAT CAT ACT GTG	336
Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val	
100 105 110	
CGC CTG ATC CGC GTC ACA GCA TCA CCC TCA GCA TGA	372
Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala	
115 120	

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Pro Asn Asn Thr Gly Lys Gln Gln Lys Arg Lys Lys Gly Asp Gly
1 5 10 15
Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala His
20 25 30
Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys
35 40 45
Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg
50 55 60
His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln
65 70 75 80
Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly
85 90 95
Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val
100 105 110
Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala
115 120

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Lelystad

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGGCCGGTA AAAACCAGAG CCAGAAGAAA AAGAAAAGTA CAGCTCCGAT GGGGAATGGC

CAGCCAGTCA ATCAACTGTG CCAGTTGCTG GGTGCAATGA TAAAGTCCCA GCGCCAGCAA	120
CCTAGGGGAG GACAGGCCAA AAAGAAAAAG CCTGAGAAGC CACATTTTCC CCTGGCTGCT	180
GAAGATGACA TCCGGCACCA CCTCACCCAG ACTGAACGCT CCCTCTGCTT GCAATCGATC	240
CAGACGGCTT TCAATCAAGG CGCAGGAACT GCGTCGCTTT CATCCAGCGG GAAGGTCAGT	300
TTTCAGGTTG AGTTTATGCT GCCGGTTGCT CATACAGTGC GCCTGATTCTG CGTGACTTCT	360
ACATCCGCCA GTCAGGGTGC AAGTTAA	387

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGGGCTGGCA TTCTTGAGGC ATCCCAGTGT TTGAATTGGA AGAATGCGTG GTGAATGGCA	60
CTGATTGACA TTGTGCCTCT AAGTCACCTA TTCAATTAGG GCGACCGTGT GGGGGTAAGA	120
TTTAATTGGC GAGAACCACA CGGCCGAAAT TAAAAA AAAA	164

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Lelystad

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTTGACAGTC AGGTGAATGG CCGCGATTGG CGTGTGGCCT CTGAGTCACC TATTCAATTA	60
GGGCGATCAC ATGGGGGTCA TACTTAATCA GGCAGGAACC ATGTGACCGA AATTAAAAAA	120
AAAAAAA	127

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid;

- (A) DESCRIPTION: DNA (synthetic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Lelystad

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTCGTCAAGT ATGGCCGGT	19
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(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid;

- (A) DESCRIPTION: DNA (synthetic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine reproductive and respiratory syndrome virus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCCATTCGCC TGACTGTCA	19
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(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other nucleic acid;
 - (A) DESCRIPTION: DNA (synthetic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porcine reproductive and respiratory syndrome virus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTGACGAGGA CTTCGGCTG

19

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other nucleic acid;
 - (A) DESCRIPTION: DNA (synthetic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porcine reproductive and respiratory syndrome virus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCTCTACCTG CAATTCTGTG

20

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other nucleic acid;
 - (A) DESCRIPTION: DNA (synthetic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porcine reproductive and respiratory syndrome virus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTGTATAGGA CCGGCAACAG

20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid;

(A) DESCRIPTION: DNA (synthetic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porcine reproductive and respiratory syndrome virus

(B) STRAIN: Iowa

(C) INDIVIDUAL ISOLATE: ISU-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGGGATCCGG TATTTGGCAA TGTGTC

26

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid;

(A) DESCRIPTION: DNA (synthetic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porcine reproductive and respiratory syndrome virus

(B) STRAIN: Iowa

(C) INDIVIDUAL ISOLATE: ISU-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGTGTTTTCC ACGAGAACCG CTTAAGGG

28

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid;

(A) DESCRIPTION: DNA (synthetic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGGGATCCAG AGTTTCAGCG G

21

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid;

(A) DESCRIPTION: DNA (synthetic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAGTTAGTCG ACACGGTCTT AAGGG

25

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other nucleic acid;
 - (A) DESCRIPTION: DNA (synthetic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porcine reproductive and respiratory syndrome virus
 - (B) STRAIN: Iowa
 - (C) INDIVIDUAL ISOLATE: ISU-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGGGATCCTT GTTAAATATG CC

22

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other nucleic acid;
 - (A) DESCRIPTION: DNA (synthetic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porcine reproductive and respiratory syndrome virus
 - (B) STRAIN: Iowa
 - (C) INDIVIDUAL ISOLATE: ISU-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTTACGCACC ACTTAAGGG

19

IN THE CLAIMS

In Claim 31 please replace "ISU-1327" with --ISU-3927--.

Please cancel Claim 32 without prejudice or disclaimer.

Please amend Claim 34 as follows:

34. (Amended) A vaccine which protects a pig against porcine reproductive and respiratory syndrome (PRRS), comprising [a] an inactivated or attenuated virus prepared by serial passage in cell culture and a physiologically acceptable carrier, wherein prior to inactivation or attenuation, said virus is the virus of Claim 31.

SUPPORT FOR THE AMENDMENTS

Support for the amendment to Claim 31 can be found in the specification at least at page 108, lines 2-3. Support for the amendment to Claim 34 can be found in the specification at page 27, lines 1-6. No new matter has been added.

REMARKS

Claims 31 and 33-41 are presently under consideration in this application.

Reconsideration is respectfully requested.

The present invention is directed to isolated viruses which cause porcine reproductive and respiratory syndrome (PRRS), and to vaccines containing the isolated viruses which protect pigs against PRRS infection, which protection can be seen as decreased number and severity of lung lesions, calculated as an average or a mean "clinical respiratory score."

The rejection of Claim 32 under 35 U.S.C. §112, fourth paragraph is rendered moot by the cancellation of Claim 32.

The rejection of Claims 36 and 38-41 under 35 U.S.C. §112, second paragraph is respectfully traversed.

The Examiner rejected Claims 38-41 for the phrase "pig in need of protection", stating that it is not clear what defines a pig in need of protection. It is noted that claims issued in the parent application, U.S. Serial No. 08/131,625, which issued December 9, 1997 as U.S. Patent No. 5,695,766 ("the '766 patent") which contained the identical phrase. Specifically, Claim 11 of the '766 patent is identical to Claim 38 except for the specific claim from which it depends. Applicants submit that the meaning of a pig in need of protection is clear from the background of the invention which describes the susceptibility to infection of swine herds in North America and Europe to strains of PRRS. Moreover, the detailed description beginning at page 14 of the specification clearly describes what is meant by a porcine respiratory and reproductive disease. Applicants submit that it is clear that a pig in need of protection from such a disease is any pig which would come into contact with the virus isolates of the present invention.

With respect to the rejection of Claim 36 for the use of "average clinical respiratory score" it is noted that Claim 9 of the '766 patent is identical to present Claim 36 except for the recitation of the specific claim from which it depends, and thus contains the recitation of "average clinical respiratory score." Moreover, there is a detailed discussion of what constitutes an "average clinical respiratory score" beginning at page 105 of the specification and continuing through Table 16 on page 107 of the specification:

In addition, each group of pigs was examined for respiratory distress according to the clinical respiratory scoring system described above (see "Clinical score mean" in Table 16 below). "Gross score" refers to the gross lung lesion score described above. "Enceph.", "myocard." and "rhinitis" refer to the number of pigs in each group exhibiting lesions of encephalitis, myocarditis and rhinitis, respectively. "Micro score" refers to a score based on the following scale, used

to evaluate and compare microscopic lesions of interstitial pneumonia in lung tissue:

- 0 = no disease; normal lung tissue
- 1 = mild multifocal microscopic lesions
- 2 = mild diffuse microscopic lesions
- 3 = moderate multifocal microscopic lesions
- 4 = moderate diffuse microscopic lesions
- 5 = severe multifocal microscopic lesions
- 6 = severe diffuse microscopic lesions

In light of the foregoing, withdrawal of this rejection is respectfully requested.

The rejection of Claims 31-41 under 35 U.S.C. §112, first paragraph for compliance with the deposit requirements is respectfully traversed.

Strains ISU-51, ISU-55 and ISU-3927 were deposited on September 29, 1993 with the American Type Culture Collection (ATCC), 12301 Parklawn Drive, Rockville, Maryland 20852 USA, as VR 2428, VR 2430 and VR 2431, respectively, in accordance with the Budapest Treaty. ISU-1894 was deposited with the ATCC on August 31, 1994 as VR 2475 in accordance with the Budapest Treaty. Deposited strains ISU-51, ISU-55, ISU-3927 and ISU-1894 are the same virus strains as identified in the above-identified application. Access to the cultures will be available during pendency of the patent application to one determined by the Commissioner to be entitled thereto under 37 C.F.R. §1.14 and 35 U.S.C. §122. All restrictions on the availability to the public of the cultures so deposited will be irrevocably removed upon the granting of the patent. The Assignee will maintain the deposited cultures and will refurnish such cultures should they become non-viable while on deposit. The deposited cultures will be maintained at said depository for a period of at least five years after the most recent request for the furnishing of a sample of the deposited culture was received by the depository, and, in any case, for a period of at least thirty (30) years after the date of the deposit, or during the enforceable life of the patent, which ever is later. In light of the

foregoing, withdrawal of the rejection under 35 U.S.C. §112, first paragraph is respectfully requested.

The rejection of Claims 36-41 under 35 U.S.C. §112, first paragraph is respectfully traversed.

The Examiner alleges that the specification does not provide sufficient guidance as to how to make attenuated viruses that are useful as a vaccine. Again, the Examiner will note that Claims 36-41 are identical to Claims 9-14 of the '766 patent in view of the amendment of Claim 34 in accordance with Claim 7 of the '766 patent, except for recitation of the specific claim from which each depends. Applicants are incorporating herein the following discussion which was presented during the prosecution of the application which issued as the '766 patent for the Examiner's convenience.

One of ordinary skill in the art at the time the present application was filed would have been familiar with the various techniques available for attenuating viruses, in particular by serial passage.

Submitted herewith are the following documents which demonstrate that methods for producing attenuated viruses by serial passage were well known in the art:

1. Britton et al (1993) *Advances in Experimental Medicine and Biology* 342:29-34;
and

2. Cubero et al (1992) *J. Comp. Path.* 106:61-70.

In addition, also submitted herewith is an Abstract from the 1996 International Pig Veterinary Society Congress (Mengelin et al) which discusses attenuation of the NADC-8 PRRSV strain as a function of cell culture passage.

Thus, methods for obtaining attenuated viruses were well known in the art at the time the application was filed, and subsequently, investigators have demonstrated that the PRRSV viruses of the present invention can be attenuated in like manner.

Furthermore, studies by one of the Assignees of the present invention have demonstrated that attenuated PRRSV strains are useful as vaccines, protecting pigs by decreasing the percentage of gross lung lesions following inoculation with unattenuated virus.

Normal, commercial, 4 week old pigs were inoculated intranasally with a targeted $10^{5.0}$ dose of each passage (p) with gross lung lesions scores obtained at 10 days post inoculation to evaluate the efficacy of this attenuated virus as a vaccine. Eight healthy PRRSV-seronegative pigs 3-5 weeks in age were vaccinated at day 0 with 22 mls of MLV ISU-55 50/preservative at a vaccine dose of 1.0×10^6 TCID₅₀ in a 2 ml volume given intranasally. Pigs were necropsied at day 45 (10 DPI) and gross lung lesion scores were determined. To monitor vaccine virus shedding, 4 sentinels were housed with vaccinates 48 hours post-vaccination. Sentinels were bled and monitored for seroconversion and viremia. Sentinels were necropsied on day 35 and gross lung lesion scores were determined. Gross lung lesion scores decrease with increased passage as follows:

Virus	% of pigs with fever $>105^{\circ}\text{C}$	Gross lung lesion scores
ISU-12 p6	20%	34.7%
ISU-12 p31	20%	12.0%
ISU-12 p56	40%	9.8%
ISU-12 p87	0%	0.8%
None	0%	1.9%

ISU-55 p50 vaccinated animals were significantly protected ($p < 0.006$) from subsequent challenge with a high virulent PRRSV isolate ISU-12 p6 as measured by GLL from non-vaccinated challenge control pigs (see attached Table). Average GLL for ISU-55 vaccinated pigs was 13% compared to challenge control scores of 32.9%. Non-challenge control pigs had an average GLL score of 5.4%. Sentinels placed with the vaccinates seroconverted by day 21 DPI but no virus was detected in sera from the sentinels. GLL scores on day 35 from sentinels was not significantly different from the non-challenge controls. These results demonstrate the efficacy of ISU-55 p50 as a modified-live virus vaccine against PRRS since vaccination was able to protect against subsequent challenge with a high virulence isolate. In addition, the vaccine virus showed some limited virus shedding which was highly desirable in that surrounding sentinels were able to obtain PRRSV antibody titers but did not induce gross lung lesions.

Thus, Applicants have shown that the attenuated viruses of the present invention do provide a protective effect to animals inoculated with wild-type virus. There is no reason to believe that the remaining strains of virus of the invention would not likewise be attenuated by serial passage and provide a protective effect to inoculated pigs.

Thus, withdrawal of this rejection is respectfully requested.

With respect to the requirement for compliance with the sequence listing requirements, Applicants submit herewith a request for preparation of a Sequence Listing from the parent application.

Applicants submit that the present application is now in condition for allowance.

Early notification to that affect is earnestly solicited.

Respectfully submitted,

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